CRF Errors Corrected by the STIC Systems Branch

Serial Number: _10/004,201_

ENTERED

OIPE ~~STIC~~

CRF Processing Date: _4/5/2002_
Edited by: _____
Verified by: _____ (STIC staff)

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically. _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____ .

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [x] Deleted: [x] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____ .

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [ ] Other: _____
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 04/05/2002
PATENT APPLICATION: US/10/004,201   TIME: 19:41:27

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04052002\J004201.raw

P.6

```
   4 <110> APPLICANT: Bornaes, Claus
   5        Andersen, Kim Vilbour
   6        Rasmussen, Poul Baad
   7        Pedersen, Anders Hjelholt
  10 <120> TITLE OF INVENTION: NEW MULTIMERIC INTERFERON BETA
  11        POLYPEPTIDES
  13 <130> FILE REFERENCE: 0220us210
  15 <140> CURRENT APPLICATION NUMBER: US 10/004,201
C--> 16 <141> CURRENT FILING DATE: 2002-03-19
  18 <150> PRIOR APPLICATION NUMBER: US 60/245,645
  19 <151> PRIOR FILING DATE: 2000-11-02
  21 <160> NUMBER OF SEQ ID NOS: 39
  23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  25 <210> SEQ ID NO: 1
  26 <211> LENGTH: 840
  27 <212> TYPE: DNA
  28 <213> ORGANISM: Homo sapiens
  30 <220> FEATURE:
  31 <221> NAME/KEY: CDS
  32 <222> LOCATION: (76)...(636)
  34 <221> NAME/KEY: sig_peptide
  35 <222> LOCATION: (76)...(138)
W--> 37 <221> mat_peptide
  38 <222> LOCATION: (139)...(636)
W--> 40 <400> 1
  41 acattctaac tgcaaccttt cgaagccttt gctctggcac aacaggtagt aggcgacact 60
  42 gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg 111
  43               Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
  44                -20                    -15                    -10
  46 ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
  47 Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
  48             -5                 1                  5
  50 ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
  51 Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
  52         10                 15                 20
  54 ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
  55 Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
  56      25                 30                 35
  58 atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
  59 Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
  60   40                 45                 50                 55
  62 gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
  63 Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
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 64                      60                   65                      70
 66 caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc  399
 67 Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
 68             75                   80                   85
 70 ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa  447
 71 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
 72         90                   95                   100
 74 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt  495
 75 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
 76     105                  110                   115
 78 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc  543
 79 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
 80 120                  125                   130                   135
 82 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta  591
 83 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
 84             140                  145                   150
 86 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac  636
 87 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 88             155                  160                   165
 90 tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca 696
 91 gcagatgctg tttaagtgac tgatggctaa tgtactgcat atgaaaggac actagaagat 756
 92 tttgaaattt ttattaaatt atgagttatt tttatttatt taaattttat tttggaaaat 816
 93 aaattatttt tggtgcaaaa gtca                                        840
 95 <210> SEQ ID NO: 2
 96 <211> LENGTH: 187
 97 <212> TYPE: PRT
 98 <213> ORGANISM: Homo sapiens
100 <220> FEATURE:
101 <221> NAME/KEY: SIGNAL
102 <222> LOCATION: (1)...(21)
104 <221> NAME/KEY: CHAIN
105 <222> LOCATION: (22)...(187)
W--> 107 <400> 2
108 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
109     -20                  -15                  -10
110 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
111 -5                   1                    5                    10
112 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
113             15                   20                   25
114 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
115         30                   35                   40
116 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
117     45                   50                   55
118 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
119 60                   65                   70                   75
120 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
121             80                   85                   90
122 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
123             95                   100                  105
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124 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
125         110                 115             120
126 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
127         125                 130             135
128 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
129 140                 145                 150                 155
130 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
131                 160                 165
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 614
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Synthetic construct
W--> 142 <221> NAME/KEY: CDS
143 <222> LOCATION: (25)...(585)
W--> 145 <221> sig_peptide
146 <222> LOCATION: (25)...(87)
W--> 148 <221> mat_peptide
149 <222> LOCATION: (88)...(585)
W--> 151 <400> 3
152 cgtttaaact taagcttcgc cacc atg acc aac aag tgc ctg ctc cag atc      51
153                               Met Thr Asn Lys Cys Leu Leu Gln Ile
154                               -20                 -15
156 gcc ctg ctc ctg tgc ttc agc acc acg gcc cta tcg atg agc tac aac    99
157 Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn
158         -10                 -5                  1
160 ctg ctc ggc ttc ctg cag agg agt tcg aac ttc cag tgc cag aag ctc   147
161 Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu
162   5                 10                  15                  20
164 ctg tgg cag ctg aac ggg cgc ctg gag tac tgc ctg aag gac agg atg   195
165 Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met
166                 25                  30                  35
168 aac ttc gac atc ccc gag gaa atc aag cag ctg cag cag ttc cag aag   243
169 Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys
170                 40                  45                  50
172 gag gac gcc gct ctg acc atc tac gag atg ctg cag aac atc ttc gcc   291
173 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala
174             55                  60                  65
176 atc ttc cgc cag gac tcc agc tcc acc ggt tgg aac gag acc atc gtg   339
177 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
178         70                  75                  80
180 gag aac ctg ctg gcc aac gtg tac cac cag atc aac cac ctg aag acc   387
181 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr
182   85                  90                  95                  100
184 gtg ctg gag gag aag ctg gag aag gag gac ttc acc cgc ggc aag ctg   435
185 Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu
186                 105                 110                 115
188 atg agc tcc ctg cac ctg aag cgc tac tat ggc cgc atc ctg cac tac   483
```

RAW SEQUENCE LISTING   DATE: 04/05/2002
PATENT APPLICATION: US/10/004,201   TIME: 19:41:27

              Input Set : A:\PTO.AMC.txt
              Output Set: N:\CRF3\04052002\J004201.raw

189 Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr
190   120   125   130
192 ctg aag gcc aag gag tac agc cac tgc gcc tgg acc atc gta cgc gtg   531
193 Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
194   135   140   145
196 gag atc ctg cgc aac ttc tac ttc atc aac cgc ctg acc ggc tac ctg   579
197 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu
198   150   155   160
200 cgc aac tgataaggat ccactagtcc agtgtggtg   614
201 Arg Asn
202 165
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 4
207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Synthetic construct
W--> 213 <221> NAME/KEY: VARIANT
214 <222> LOCATION: 4
215 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 217 <400> 4
W--> 218 Ile Asn Ala Xaa
219 1
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 4
224 <212> TYPE: PRT
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Synthetic construct
W--> 230 <221> NAME/KEY: VARIANT
231 <222> LOCATION: 4
232 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 234 <400> 5
W--> 235 Gly Asn Ile Xaa
236 1
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 4
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Synthetic construct
W--> 247 <221> NAME/KEY: VARIANT
248 <222> LOCATION: 4
249 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 251 <400> 6
W--> 252 Val Asn Ile Xaa
253 1
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 4

RAW SEQUENCE LISTING   DATE: 04/05/2002
PATENT APPLICATION: US/10/004,201   TIME: 19:41:27

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04052002\J004201.raw

```
        258 <212> TYPE: PRT
        259 <213> ORGANISM: Artificial Sequence
        261 <220> FEATURE:
        262 <223> OTHER INFORMATION: Synthetic construct
W--> 264 <221> NAME/KEY: VARIANT
        265 <222> LOCATION: 4
        266 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 268 <400> 7
W--> 269 Ser Asn Ile Xaa
        270  1
        273 <210> SEQ ID NO: 8
        274 <211> LENGTH: 5
        275 <212> TYPE: PRT
        276 <213> ORGANISM: Artificial Sequence
        278 <220> FEATURE:
        279 <223> OTHER INFORMATION: Synthetic construct
W--> 281 <221> NAME/KEY: VARIANT
        282 <222> LOCATION: 5
        283 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 285 <400> 8
W--> 286 Ala Ser Asn Ile Xaa
        287  1               5
        290 <210> SEQ ID NO: 9
        291 <211> LENGTH: 6
        292 <212> TYPE: PRT
        293 <213> ORGANISM: Artificial Sequence
        295 <220> FEATURE:
        296 <223> OTHER INFORMATION: Synthetic construct
W--> 298 <221> NAME/KEY: VARIANT
        299 <222> LOCATION: 6
        300 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 302 <400> 9
W--> 303 Ser Pro Ile Asn Ala Xaa
        304  1               5
        307 <210> SEQ ID NO: 10
        308 <211> LENGTH: 7
        309 <212> TYPE: PRT
        310 <213> ORGANISM: Artificial Sequence
        312 <220> FEATURE:
        313 <223> OTHER INFORMATION: Synthetic construct
W--> 315 <221> NAME/KEY: VARIANT
        316 <222> LOCATION: 7
        317 <223> OTHER INFORMATION: Xaa = Thr or Ser
W--> 319 <400> 10
W--> 320 Ala Ser Pro Ile Asn Ala Xaa
        321  1               5
        324 <210> SEQ ID NO: 11
        325 <211> LENGTH: 11
        326 <212> TYPE: PRT
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/05/2002
PATENT APPLICATION: US/10/004,201   TIME: 19:41:28

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04052002\J004201.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 4
Seq#:5; Xaa Pos. 4
Seq#:6; Xaa Pos. 4
Seq#:7; Xaa Pos. 4
Seq#:8; Xaa Pos. 5
Seq#:9; Xaa Pos. 6
Seq#:10; Xaa Pos. 7
Seq#:11; Xaa Pos. 4,8
Seq#:12; Xaa Pos. 4,9,14